W635

Supporting California Condor Conservation Management Through Analysis of Species-wide Whole Genome Sequence Variation

Date: Saturday, January 11, 2014
Time: 5:00 PM
Room: Pacific Salon 3

Oliver Ryder *, San Diego Zoo Institute for Conservation Research, Escondido, CA*
Leona G. Chemnick , San Diego Zoo Institute for Conservation Research
Steven Thomas , San Diego Zoo Institute for Conservation Research
Jessica Martin , Mississippi State University
Michael Romanov , University of Kent, Canterbury CT2, United Kingdom
Katherine Ralls , Smithsonian Conservation Biology Institute, Washington, DC
Jonathan D. Ballou , Center for Conservation and Evolutionary Genetics, Washington, DC
Michael Mace , San Diego Zoo Safari Park, San Diego, CA
Aakrosh Ratan , Pennsylvania State University
Webb Miller , Pennsylvania State University, Pennsylvania, PA
Stephan Schuster , Pennsylvania State University

The critically endangered California condor (*Gymnogyps californianus*) has been the focus of intensive conservation efforts for several decades. Reduced to a population size of twenty-three birds in 1985, the entire surviving population was brought under captive management for recovery. Founded by fourteen individuals, the surviving California condor gene pool has been managed through captive breeding of individuals paired through pedigree analysis. As of August, 2013, there were 424 California condor individuals; 223 are flying in the wild in four re-introduced populations in California, Arizona and Baja California, Mexico. All condors have their sex identified via amplification of sex chromosome specific markers and DNA samples are stored for every individual of the species. Microsatellite genotyping has confirmed parentage in captive and wild condor chicks, corrected switched identities, and identified successful extra-pair copulation in the wild population. Whole genome sequencing using data generated on multiple platforms has been used to produce a de novo genome assembly for a founder male condor and thirty additional condors that together encompass the entire genetic variation of the species, perhaps the first time such a comprehensive effort has been conducted for any species. Studbook-based kinship relationships between founder birds and kinship estimates from genome-wide genetic variation can be compared and evaluated in the context of retention of genetic diversity in the generations of California condors. Genomic studies of California condors are providing a model system for avian conservation genomics and allow empirical evaluation of basic facets of transmission genetics, including segregation, linkage, recombination and mutation.

Back to: Population & Conservation Genomics

<< Previous Abstract | Next Abstract >>

Home/Search
Browse by Day
Browse by Type
Author Index
Poster Categories

Meeting Information

When:
January 10 - 15, 2014
Where:
San Diego, CA